

EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	0	("(GeorgeNCox).inv.").PN.	US-PGPUB; USPAT; EPO; JPO	OR	OFF	2006/09/26 21:29
L2	40	(george N Cox).inv.	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	OFF	2006/09/26 21:29
S1	117	(interleukin-11).clm.	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	OFF	2006/09/26 21:29
S2	10	(interleukin-11 PEG).clm.	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	OFF	2006/09/25 12:39
S3	1	("6608183").PN.	US-PGPUB; USPAT; EPO; JPO	OR	OFF	2006/09/25 13:00
S4	1	("5206344").PN.	US-PGPUB; USPAT; EPO; JPO	OR	OFF	2006/09/25 13:01
S5	1	("5166322").PN.	US-PGPUB; USPAT; EPO; JPO	OR	OFF	2006/09/25 13:01
S6	4	(interleukin-11 cysteine added variant).clm.	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	OFF	2006/09/25 14:21
S7	5	(interleukin-11 cysteine variant).clm.	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	OFF	2006/09/25 14:21

(FILE 'HOME' ENTERED AT 21:49:49 ON 26 SEP 2006)

FILE 'MEDLINE, BIOSIS, EMBASE, CAPLUS' ENTERED AT 21:50:02 ON 26 SEP 2006

L1 86 S COX G N/AU
L2 43 DUP REM L1 (43 DUPLICATES REMOVED)
L3 4345 S IL-11
L4 3 S (CYSTEINE ADDED VARIANT)
L5 0 S L3 AND L4
L6 8664 S PEGYLATED
L7 16 S L3 AND L6
L8 7 DUP REM L7 (9 DUPLICATES REMOVED)
L9 0 S (IL-11 VARIANT)
L10 0 S (IL-11 PEG)
L11 16 S (IL-11 AND PEG)
L12 8 DUP REM L11 (8 DUPLICATES REMOVED)
L13 0 S (PEG-IL11)
L14 0 S (IL-11 AND PEG AND VARIANT)
L15 3 S L1 AND L6

=> logoff

SCORE Search Results Details for Application 10773939 and Search Result us-10-773-939-17.rag.

Comments /
Suggestions

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OM protein - protein search, using sw model

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Run on:      September 21, 2006, 09:55:14 ; Search time 198 Seconds
              (without alignments)
              459.526 Million cell updates/sec
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Title:          US-10-773-939-17
Perfect score: 1025
Sequence:      1 MNCVCRLVLVVLSLWPDTAV.....GLHLTLDWAVRGLLLLKTRL 199
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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5:  geneseqp2002s:*
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7:  geneseqp2003bs:*
8:  geneseqp2004s:*
9:  geneseqp2005s:*
10: geneseqp2006s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1025	100.0	199	2	AAR12314	Aar12314 Human int
2	1025	100.0	199	2	AAR50176	Aar50176 Human Int
3	1025	100.0	199	3	AAy87815	Aay87815 Human IL-
4	1025	100.0	199	5	AAU78377	Aau78377 Human int
5	1025	100.0	199	6	ABU09747	Abu09747 Human int
6	1025	100.0	199	7	ADC78851	Adc78851 Human PRO
7	1025	100.0	199	7	ADF70854	Adf70854 Human int
8	1025	100.0	199	8	ADL16724	Adl16724 Human int
9	1025	100.0	199	8	ADQ19047	Adq19047 Human sof
10	1025	100.0	199	9	ADX16342	Adx16342 Full leng
11	1025	100.0	199	9	ADY93813	Ady93813 Human int
12	1022	99.7	199	2	AAR24436	Aar24436 Sequence
13	1009	98.4	199	9	ADX16360	Adx16360 Full leng
14	1007	98.2	199	9	ADX16364	Adx16364 Full leng
15	1006	98.1	199	9	ADX16361	Adx16361 Full leng
16	1006	98.1	199	9	ADX16362	Adx16362 Full leng
17	1005	98.0	199	9	ADX16363	Adx16363 Full leng
18	1003	97.9	199	2	AAR43260	Aar43260 Human adi
19	963	94.0	199	2	AAR12313	Aar12313 Primate i
20	963	94.0	199	9	ADX16343	Adx16343 Full leng
21	947	92.4	199	9	ADX16375	Adx16375 Full leng
22	945	92.2	199	9	ADX16379	Adx16379 Full leng
23	944	92.1	199	9	ADX16377	Adx16377 Full leng
24	944	92.1	199	9	ADX16376	Adx16376 Full leng
25	943	92.0	199	9	ADX16378	Adx16378 Full leng
26	927	90.4	546	9	AEE03556	Aee03556 Human sIL
27	927	90.4	546	9	AEE39539	Aee39539 Novel des
28	926	90.3	181	9	AEE03555	Aee03555 Human IL-
29	926	90.3	181	9	AEE39538	Aee39538 Human mat
30	914	89.2	178	2	AAR75337	Aar75337 Human int
31	914	89.2	178	2	AAW02202	Aaw02202 Human int
32	914	89.2	763	8	ADL16712	Adl16712 Human stu
33	914	89.2	763	9	AEA61939	Aea61939 Albumin-i
34	914	89.2	787	9	AEA61938	Aea61938 Albumin-i
35	907	88.5	296	2	AAR26213	Aar26213 Fusion pr
36	907	88.5	296	2	AAR26051	Aar26051 Thioredox
37	907	88.5	296	2	AAR45916	Aar45916 E.coli th
38	907	88.5	296	2	AAR50177	Aar50177 Thioredox
39	907	88.5	296	2	AAR75762	Aar75762 Thioredox
40	907	88.5	296	2	AAR76812	Aar76812 Thioredox
41	907	88.5	762	9	AEA61936	Aea61936 Interleuk
42	907	88.5	786	9	AEA61935	Aea61935 Interleuk
43	905	88.3	264	2	AAW53324	Aaw53324 P-selecti
44	905	88.3	264	2	AAy29769	Aay29769 Human P-s
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ALIGNMENTS

RESULT 1

AAR12314

ID AAR12314 standard; protein; 199 AA.

XX

AC AAR12314;

XX

DT 25-MAR-2003 (revised)

SCORE Search Results Details for Application 10773939 and Search Result us-10-773-939-17.ra1.

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OM protein - protein search, using sw model

Run on: September 21, 2006, 10:04:03 ; Search time 49 Seconds
(without alignments)
355.482 Million cell updates/sec

Title: US-10-773-939-17
Perfect score: 1025
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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No.	Score	Match Length	DB	ID			Description

1	1025	100.0	199	1	US-08-017-522A-4	Sequence 4, Appli
2	1025	100.0	199	1	US-08-115-680-2	Sequence 2, Appli
3	1025	100.0	199	1	US-07-941-372-2	Sequence 2, Appli
4	1025	100.0	199	1	US-07-949-516A-4	Sequence 4, Appli
5	1025	100.0	199	1	US-08-792-019B-8	Sequence 8, Appli
6	1025	100.0	199	1	US-08-814-459-4	Sequence 4, Appli
7	1025	100.0	199	2	US-08-988-819-8	Sequence 8, Appli
8	1025	100.0	199	2	US-09-122-525-4	Sequence 4, Appli
9	1025	100.0	199	2	US-09-016-534-8	Sequence 8, Appli
10	1025	100.0	199	2	US-09-462-941-17	Sequence 17, Appl
11	1025	100.0	199	2	US-09-949-016-5975	Sequence 5975, Ap
12	1025	100.0	199	5	PCT-US93-08247-2	Sequence 2, Appli
13	1025	100.0	220	2	US-09-949-016-10269	Sequence 10269, A
14	963	94.0	199	1	US-08-017-522A-2	Sequence 2, Appli
15	963	94.0	199	1	US-07-949-516A-2	Sequence 2, Appli
16	963	94.0	199	1	US-08-814-459-2	Sequence 2, Appli
17	963	94.0	199	2	US-09-122-525-2	Sequence 2, Appli
18	963	94.0	199	7	5215895-3	Patent No. 5215895
19	963	94.0	199	7	5215895-4	Patent No. 5215895
20	907	88.5	296	1	US-07-745-382-14	Sequence 14, Appl
21	907	88.5	296	1	US-07-921-848-14	Sequence 14, Appl
22	907	88.5	296	1	US-08-115-680-4	Sequence 4, Appli
23	907	88.5	296	1	US-07-941-372-4	Sequence 4, Appli
24	907	88.5	296	1	US-08-165-301A-14	Sequence 14, Appl
25	907	88.5	296	2	US-08-810-436-14	Sequence 14, Appl
26	907	88.5	296	5	PCT-US93-08247-4	Sequence 4, Appli
27	907	88.5	296	5	PCT-US94-14179-14	Sequence 14, Appl
28	905	88.3	264	2	US-08-713-556F-42	Sequence 42, Appl
29	276.5	27.0	176	2	US-08-149-101A-26	Sequence 26, Appl
30	276.5	27.0	176	5	PCT-US94-12873-26	Sequence 26, Appl
31	232	22.6	191	2	US-08-149-101A-24	Sequence 24, Appl
32	232	22.6	191	5	PCT-US94-12873-24	Sequence 24, Appl
33	227	22.1	182	2	US-08-149-101A-25	Sequence 25, Appl
34	227	22.1	182	5	PCT-US94-12873-25	Sequence 25, Appl
35	109	10.6	373	2	US-09-252-991A-29300	Sequence 29300, A
36	106	10.3	827	3	US-10-171-384-3	Sequence 3, Appli
37	103.5	10.1	620	2	US-09-270-767-46214	Sequence 46214, A
38	102.5	10.0	4551	2	US-09-320-878-1	Sequence 1, Appli
39	102.5	10.0	4551	2	US-09-141-908-2	Sequence 2, Appli
40	102.5	10.0	4551	2	US-09-657-440-1	Sequence 1, Appli
41	102.5	10.0	4551	2	US-09-793-708-1	Sequence 1, Appli
42	102.5	10.0	4613	2	US-09-105-537-31	Sequence 31, Appl
43	102.5	10.0	11877	2	US-09-105-537-6	Sequence 6, Appli
44	101	9.9	218	2	US-09-893-737-28	Sequence 28, Appl
45	100.5	9.8	1089	2	US-10-012-231A-102	Sequence 102, App

ALIGNMENTS

RESULT 1

US-08-017-522A-4

; Sequence 4, Application US/08017522A

; Patent No. 5371193

; GENERAL INFORMATION:

; APPLICANT: BENNETT, FRANCES K

; APPLICANT: PAUL, STEPHAN R

; APPLICANT: YANG, YU-CHUNG

; TITLE OF INVENTION: A MAMMALIAN CYTOKINE, IL-11

; NUMBER OF SEQUENCES: 4

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OM protein - protein search, using sw model

Run on: September 21, 2006, 10:04:41 ; Search time 172 Seconds
(without alignments)
535.929 Million cell updates/sec

Title: US-10-773-939-17
Perfect score: 1025
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	1025	100.0	199	3 US-09-791-497-5	Sequence 5, Appli

2	1025	100.0	199	3	US-09-825-751A-80	Sequence 80, Appl
3	1025	100.0	199	4	US-10-400-377-17	Sequence 17, Appl
4	1025	100.0	199	4	US-10-400-708-17	Sequence 17, Appl
5	1025	100.0	199	4	US-10-298-148-17	Sequence 17, Appl
6	1025	100.0	199	4	US-10-609-346-14	Sequence 14, Appl
7	1025	100.0	199	4	US-10-773-939-17	Sequence 17, Appl
8	1025	100.0	199	4	US-10-774-149-17	Sequence 17, Appl
9	1025	100.0	199	4	US-10-773-654-17	Sequence 17, Appl
10	1025	100.0	199	5	US-10-866-540-17	Sequence 17, Appl
11	1025	100.0	199	5	US-10-723-860-1866	Sequence 1866, Ap
12	1025	100.0	199	5	US-10-856-219-17	Sequence 17, Appl
13	1025	100.0	199	5	US-10-685-288-17	Sequence 17, Appl
14	1025	100.0	199	5	US-10-491-997-80	Sequence 80, Appl
15	1025	100.0	199	5	US-10-866-580-17	Sequence 17, Appl
16	1025	100.0	199	5	US-10-773-530-17	Sequence 17, Appl
17	1025	100.0	199	5	US-10-851-438-80	Sequence 80, Appl
18	1025	100.0	199	6	US-11-071-098-17	Sequence 17, Appl
19	1025	100.0	199	6	US-11-070-993-17	Sequence 17, Appl
20	914	89.2	763	4	US-10-609-346-2	Sequence 2, Appli
21	905	88.3	264	3	US-09-935-144-42	Sequence 42, Appl
22	898	87.6	199	3	US-09-791-497-6	Sequence 6, Appli
23	124	12.1	616	4	US-10-103-313-460	Sequence 460, App
24	110	10.7	5432	5	US-10-760-493-31	Sequence 31, Appl
25	108	10.5	350	5	US-10-204-639-68	Sequence 68, Appl
26	107	10.4	1042	4	US-10-282-122A-61918	Sequence 61918, A
27	106	10.3	827	4	US-10-171-384-3	Sequence 3, Appli
28	105	10.2	249	4	US-10-425-115-249484	Sequence 249484,
29	103.5	10.1	399	6	US-11-097-143-4584	Sequence 4584, Ap
30	103.5	10.1	7510	5	US-10-760-493-35	Sequence 35, Appl
31	102.5	10.0	4551	3	US-09-793-708-1	Sequence 1, Appli
32	102.5	10.0	4551	4	US-10-201-365-2	Sequence 2, Appli
33	102.5	10.0	4551	4	US-10-160-539-1	Sequence 1, Appli
34	102.5	10.0	4551	5	US-10-468-828-1	Sequence 1, Appli
35	102.5	10.0	4551	5	US-10-846-335-1	Sequence 1, Appli
36	102.5	10.0	4613	3	US-09-861-289-31	Sequence 31, Appl
37	102.5	10.0	4613	3	US-09-860-846-31	Sequence 31, Appl
38	102.5	10.0	4613	3	US-09-988-384B-31	Sequence 31, Appl
39	102.5	10.0	4613	3	US-09-836-821-31	Sequence 31, Appl
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41	102.5	10.0	11877	3	US-09-861-289-6	Sequence 6, Appli
42	102.5	10.0	11877	3	US-09-860-846-6	Sequence 6, Appli
43	102.5	10.0	11877	3	US-09-836-821-6	Sequence 6, Appli
44	102.5	10.0	11877	4	US-10-271-889-49	Sequence 49, Appl
45	102.5	10.0	12199	3	US-09-988-384B-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-09-791-497-5

; Sequence 5, Application US/09791497

; Publication No. US20030008343A1

; GENERAL INFORMATION:

; APPLICANT: Timans, Jacqueline C.

; APPLICANT: Kastelein, Robert A.

; APPLICANT: Bazan, J. Fernando

; APPLICANT: Pflanz, Stefan

; TITLE OF INVENTION: Mammalian Cytokines; Related Reagents

; FILE REFERENCE: DX01040K2

; CURRENT APPLICATION NUMBER: US/09/791,497

SCORE Search Results Details for Application 10773939 and Search Result us-10-773-939-17.rapbn.

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OM protein - protein search, using sw model

Run on: September 21, 2006, 10:05:36 ; Search time 34 Seconds
(without alignments)
416.508 Million cell updates/sec

Title: US-10-773-939-17
Perfect score: 1025
Sequence: 1 MNCVCRLVLVLSLWPD TAV.....GLHLTLDWAVRGLLLLKTRL 199

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 260401 seqs, 71162236 residues

Total number of hits satisfying chosen parameters: 260401

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*

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- 2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
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- 7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result %
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No.	Score	Match	Length	DB	ID	Description
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2	110	10.7	1411	7	US-11-330-403-16307	Sequence 16307, A
3	102	10.0	306	6	US-10-953-349-35329	Sequence 35329, A
4	102	10.0	306	7	US-11-056-355B-9781	Sequence 9781, Ap
5	102	10.0	321	6	US-10-953-349-35328	Sequence 35328, A
6	102	10.0	321	7	US-11-056-355B-9780	Sequence 9780, Ap
7	102	10.0	376	6	US-10-953-349-35327	Sequence 35327, A
8	102	10.0	376	7	US-11-056-355B-9779	Sequence 9779, Ap
9	100.5	9.8	1089	6	US-10-196-749-266	Sequence 266, App
10	96	9.4	217	7	US-11-056-355B-1368	Sequence 1368, Ap
11	95.5	9.3	243	7	US-11-275-181-3	Sequence 3, Appli
12	95	9.3	599	6	US-10-449-902-47030	Sequence 47030, A
13	94.5	9.2	476	7	US-11-056-355B-16525	Sequence 16525, A
14	94.5	9.2	1036	7	US-11-248-956-2	Sequence 2, Appli
15	94.5	9.2	1036	7	US-11-121-133-255	Sequence 255, App
16	94.5	9.2	1036	7	US-11-121-133-256	Sequence 256, App
17	94	9.2	252	7	US-11-036-257-75	Sequence 75, Appl
18	92.5	9.0	206	7	US-11-056-355B-1369	Sequence 1369, Ap
19	92.5	9.0	1154	7	US-11-301-457-23	Sequence 23, Appl
20	92	9.0	933	6	US-10-526-905-15	Sequence 15, Appl
21	92	9.0	933	7	US-11-283-329-106	Sequence 106, App
22	92	9.0	1360	7	US-11-330-403-4001	Sequence 4001, Ap
23	92	9.0	3575	7	US-11-330-403-5161	Sequence 5161, Ap
24	91	8.9	614	6	US-10-449-902-51430	Sequence 51430, A
25	90.5	8.8	819	6	US-10-449-902-56721	Sequence 56721, A
26	89	8.7	265	7	US-11-056-355B-2446	Sequence 2446, Ap
27	88.5	8.6	193	7	US-11-056-355B-59910	Sequence 59910, A
28	88.5	8.6	198	7	US-11-056-355B-59909	Sequence 59909, A
29	88.5	8.6	222	7	US-11-056-355B-59908	Sequence 59908, A
30	88.5	8.6	2082	7	US-11-330-403-9531	Sequence 9531, Ap
31	87.5	8.5	154	6	US-10-953-349-38409	Sequence 38409, A
32	87.5	8.5	398	7	US-11-330-403-18597	Sequence 18597, A
33	87.5	8.5	871	7	US-11-330-403-2899	Sequence 2899, Ap
34	87	8.5	225	7	US-11-056-355B-62339	Sequence 62339, A
35	87	8.5	743	7	US-11-121-133-164	Sequence 164, App
36	87	8.5	743	7	US-11-121-133-254	Sequence 254, App
37	87	8.5	1015	6	US-10-505-928-359	Sequence 359, App
38	87	8.5	3792	7	US-11-330-623-10	Sequence 10, Appl
39	86.5	8.4	485	7	US-11-056-355B-66410	Sequence 66410, A
40	86.5	8.4	519	6	US-10-526-940-9	Sequence 9, Appli
41	86	8.4	249	7	US-11-056-355B-15700	Sequence 15700, A
42	86	8.4	404	7	US-11-056-355B-15699	Sequence 15699, A
43	86	8.4	409	7	US-11-056-355B-15698	Sequence 15698, A
44	86	8.4	481	6	US-10-449-902-29923	Sequence 29923, A
45	86	8.4	481	6	US-10-449-902-54571	Sequence 54571, A

ALIGNMENTS

RESULT 1

US-11-300-928-18

; Sequence 18, Application US/11300928

; Publication No. US20060166277A1

; GENERAL INFORMATION:

; APPLICANT: Karumanchi, S. Ananth

; APPLICANT: Sukhatme, Vikas P.

; TITLE OF INVENTION: Nucleic Acids and Polypeptides Useful For Diagnosing and Treati

; TITLE OF INVENTION: Complications of Pregnancy

5	898	87.6	199	1	IL11_RAT	Q99mf5	rattus norv
6	878	85.7	218	2	Q3V0U3_MOUSE	Q3v0u3	mus musculu
7	183.5	17.9	198	2	Q4H133_CYPCA	Q4h133	cyprinus ca
8	181.5	17.7	204	2	Q5NKG1_ONCMY	Q5nkg1	oncorhynchu
9	159	15.5	201	2	Q494Q9_FUGRU	Q494q9	fugu rubrip
10	159	15.5	219	2	Q494Q5_BRARE	Q494q5	brachydanio
11	149	14.5	1990	2	Q4SN43_TETNG	Q4sn43	tetraodon n
12	147.5	14.4	200	2	Q494Q7_TETNG	Q494q7	tetraodon n
13	120.5	11.8	194	2	Q494Q4_BRARE	Q494q4	brachydanio
14	116.5	11.4	520	2	Q80ZB8_RAT	Q80zb8	rattus norv
15	115	11.2	511	2	Q80ZB9_RAT	Q80zb9	rattus norv
16	115	11.2	837	2	Q63618_RAT	Q63618	rattus norv
17	114.5	11.2	715	2	Q725K1_DESVH	Q725k1	desulfovibr
18	111.5	10.9	320	2	Q2IG12_9DELT	Q2igl2	anaeromyxob
19	110.5	10.8	871	2	Q9ET47_MOUSE	Q9et47	mus musculu
20	110	10.7	375	2	Q4WZQ1_AS PFU	Q4wzq1	aspergillus
21	110	10.7	433	2	Q8T3H9_DROME	Q8t3h9	drosophila
22	110	10.7	1411	2	Q73Y53_MYCPA	Q73y53	mycobacteri
23	110	10.7	5432	2	Q52V52_9ACTO	Q52v52	streptomyce
24	109.5	10.7	763	1	RIN1_MOUSE	Q921q7	mus musculu
25	108.5	10.6	1755	2	Q80WC3_MOUSE	Q80wc3	mus musculu
26	108	10.5	997	2	Q3J6B6_RHOS4	Q3j6b6	rhodobacter
27	108	10.5	1243	2	Q6GQT8_MOUSE	Q6gqt8	mus musculu
28	107.5	10.5	388	2	Q9KZV7_STRCO	Q9kzv7	streptomyce
29	107	10.4	275	2	Q5Z4H2_ORYSA	Q5z4h2	oryza sativ
30	106	10.3	438	2	Q5SIW1_THET8	Q5siw1	thermus the
31	106	10.3	438	2	Q72J90_THET2	Q72j90	thermus the
32	106	10.3	828	1	IASPP_HUMAN	Q8wuf5	homo sapien
33	106	10.3	828	2	Q2PNZ9_HUMAN	Q2pnz9	homo sapien
34	106	10.3	969	2	Q4VBD6_MOUSE	Q4vbd6	mus musculu
35	105.5	10.3	571	2	Q96AX3_HUMAN	Q96ax3	homo sapien
36	105.5	10.3	871	2	Q96S23_HUMAN	Q96s23	homo sapien
37	105	10.2	1003	2	Q3TY92_MOUSE	Q3ty92	mus musculu
38	104.5	10.2	341	2	Q3W467_9ACTO	Q3w467	frankia sp.
39	104	10.1	783	2	Q9VPX6_DROME	Q9vpx6	drosophila
40	103.5	10.1	832	2	Q9VNC4_DROME	Q9vnc4	drosophila
41	103.5	10.1	1322	2	Q5K7E6_CRYNE	Q5k7e6	cryptococcu
42	103.5	10.1	7510	2	Q52V50_9ACTO	Q52v50	streptomyce
43	102.5	10.0	303	2	Q4K7J6_PSEF5	Q4k7j6	pseudomonas
44	102.5	10.0	4613	2	Q9ZGI5_9ACTO	Q9zgi5	streptomyce
45	101.5	9.9	208	2	Q6UAM0_TETNG	Q6uam0	tetraodon n

ALIGNMENTS

RESULT 1

IL11_HUMAN

ID IL11_HUMAN STANDARD; PRT; 199 AA.
AC P20809;
DT 01-FEB-1991, integrated into UniProtKB/Swiss-Prot.
DT 01-FEB-1991, sequence version 1.
DT 07-FEB-2006, entry version 55.
DE Interleukin-11 precursor (IL-11) (Adipogenesis inhibitory factor)
DE (AGIF) (Oprelvekin).
GN Name=IL11;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;